

10/2

#2

OIPE

RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/963,285

TIME: 14:02:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963285.raw

4 <110> APPLICANT: Enerbck, Sven
5 Krook, Katarina
6 Rondahl, Lena
7 Wasserman, Wyeth
9 <120> TITLE OF INVENTION: PROMOTER SEQUENCES
11 <130> FILE REFERENCE: 13425-042001
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/963,285
C--> 13 <141> CURRENT FILING DATE: 2001-09-26
13 <150> PRIOR APPLICATION NUMBER: SE 0004102-0
14 <151> PRIOR FILING DATE: 2000-11-09
16 <150> PRIOR APPLICATION NUMBER: US 60/238,897
17 <151> PRIOR FILING DATE: 2000-10-10
19 <150> PRIOR APPLICATION NUMBER: SE 0003435-5
20 <151> PRIOR FILING DATE: 2000-09-26
22 <160> NUMBER OF SEQ ID NOS: 24
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 6458
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (2235)...(3737)
35 <400> SEQUENCE: 1

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38	ggccgaagcg	aagaggcctg	gtgggttgtc	tcaacatcct	tttgctgaga	atcgaatacg	180
39	cagccgatga	acagccagga	agggtgcaag	gaaacctgaa	atacaaattg	tctccctgaa	240
40	gccctcttcc	ctgcccgaac	agaccagcaa	cttccaaaat	tctgcccgtg	tttagccttg	300
41	ttaaaggggt	gtctcactcc	ttcagggaaa	gtgggaaaag	gggatctgat	tattgaggtg	360
42	tggaaggaat	aaataatcag	tccacaaata	aacaaactgt	ccgggattcc	tagaggggaag	420
43	gagaaatcct	tgaaggagat	ccaagtcgct	ccaggtctgc	ctgccgaata	atatcatccc	480
44	gaagggatct	tgaaccgttt	gcaatcaacc	gtcacccag	tcttcccacg	gagcgcgctc	540
45	cctaactcac	cctaccaccc	caacaaaaca	aaaaaaaggc	tgaaatatag	aaaagcaact	600
46	tggaggctcc	cagggggacg	ttgccaggag	caggaggcag	ggacagcgcc	ctagggtcgg	660
47	tgttagcggc	cggcgccggc	ctgggccacg	ggaaacgtcc	acgcttggtg	cccgcggtgc	720
48	gcggcgctca	ttgcgcgcgc	cttcgagcca	agcccccgcg	gaaaacaggc	tcgggtttct	780
49	cctcgcaggg	cccaggaact	cggctctgcc	tggccccggg	gggtcgctgc	attgtcccgg	840
50	tcttctggga	gtgcgggtgc	agcttggttag	aggggaatttc	tacctgggaa	aagggagacg	900
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52	agcagagtca	cttcaccctt	ttccccaaac	cccacaaaac	tgctcgcagc	gacgcggatg	1020
53	atctaccgaa	ttccccgcga	attcggaggga	ttaagttgtc	agtcagcacg	ttgctacctt	1080
54	cccctctatg	cactccgctg	cctggtcctt	cggcggggag	cgagggaaac	tcagtttgta	1140
55	gggtttacct	ctaaaacctc	gataggttat	ccttgacgac	cccagacctg	gaaactccct	1200
56	gttgatgatt	aattatttga	ttaaataagt	ataacatcca	ggagaggccc	tgccattcca	1260
57	atccagcgcg	tttgcttttg	aatccattac	acctgggccc	ccataattag	gaaatcta	1320
58	tattcgcttc	atcactcatt	aataagaaaa	atgtcccagg	atcattgcta	cttacaaggt	1380

ENTERED

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60 ttttaacagag gaaagtggct atctttttgt tttggggcatg tgggcccatt caccaaaatg 1500
61 tgatcataaaa ataaatttta ataagatata acttttttaa aagttttcaa gtgaagacgg 1560
62 agtcgccgcg gaggccgggg cgccgggggtc ttagagccga cggattcctg cgctcctcgc 1620
63 cccgattggc gccggactcc tctcagctgc cgggtgattg gctcaaagtt ccgggagggg 1680
64 gcgtggcccg aggaaagtaa aaactcgctt tcagcaagaa gacttttgaa acttttccca 1740
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66 gcgcgctgac cctcggggct gccgattcgc tgggggcttg gagagcctcc tgcgcccctc 1860
67 ctgcgcggcg ccgagggtcc accttggctc ccaggccgcg gcgtctccgc tgggtccgcg 1920
68 gccgcccggc tgcccgcgct gccgcccggc ggtcctggag ccagcgagga gcggggcccg 1980
69 cgctgcgctt gcccggggcg cgccctccag gatgccgac cgcccgggtcc gctgaaagcg 2040
70 cgcccccctg ctgcggccga gcgacgacga ccgcgcaccc tcgccccgga ggctgccagg 2100
71 agaccggggc cgccctctcc gctccctcc tctccctctc tggtctctct gcgtctctc 2160
72 gctctcaggg cccctctcgc tccccggcc gcagtcctg cgcgaggcg ccggcgagcc 2220
73 gtctcggaag cagc atg cag gcg cgc tac tcc gtg tcc gac ccc aac gcc 2270
74 Met Gln Ala Arg Tyr Ser Val Ser Asp Pro Asn Ala
75 1 5 10
77 ctg gga gtg gtg ccc tac ctg agc gag cag aat tac tac cgg gct gcg 2318
78 Leu Gly Val Val Pro Tyr Leu Ser Glu Gln Asn Tyr Tyr Arg Ala Ala
79 15 20 25
81 ggc agc tac ggc ggc atg gcc agc ccc atg ggc gtc tat tcc ggc cac 2366
82 Gly Ser Tyr Gly Gly Met Ala Ser Pro Met Gly Val Tyr Ser Gly His
83 30 35 40
85 ccg gag cag tac agc gcg ggg atg ggc cgc tcc tac gcg ccc tac cac 2414
86 Pro Glu Gln Tyr Ser Ala Gly Met Gly Arg Ser Tyr Ala Pro Tyr His
87 45 50 55 60
89 cac cac cag ccc gcg gcg cct aag gac ctg gtg aag ccg ccc tac agc 2462
90 His His Gln Pro Ala Ala Pro Lys Asp Leu Val Lys Pro Pro Tyr Ser
91 65 70 75
93 tac atc gcg ctc atc acc atg gcc atc cag aac gcg ccc gag aag aag 2510
94 Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Glu Lys Lys
95 80 85 90
97 atc acc ttg aac ggc atc tac cag ttc atc atg gac cgc ttc ccc ttc 2558
98 Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe
99 95 100 105
101 tac cgg gag aac aag cag ggc tgg cag aac agc atc cgc cac aac ctc 2606
102 Tyr Arg Glu Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His Asn Leu
103 110 115 120
105 tcg ctc aac gag tgc ttc gtc aag gtg ccc cgc gac gac aag aag ccc 2654
106 Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys Lys Pro
107 125 130 135 140
109 ggc aag ggc agt tac tgg acc ctg gac ccg gac tcc tac aac atg ttc 2702
110 Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn Met Phe
111 145 150 155
113 gag aac ggc agc ttc ctg cgg cgc cgg cgg cgc ttc aaa aag aag gac 2750
114 Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Arg Phe Lys Lys Lys Asp
115 160 165 170
117 gtg tcc aag gag aag gag gag cgg gcc cac ctc aag gag ccg ccc ccg 2798
118 Val Ser Lys Glu Lys Glu Glu Arg Ala His Leu Lys Glu Pro Pro Pro

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119	175	180	185	
121	gcg gcg tcc aag ggc gcc ccg gcc acc ccc cac cta gcg gac gcc ccc	2846		
122	Ala Ala Ser Lys Gly Ala Pro Ala Thr Pro His Leu Ala Asp Ala Pro			
123	190 195 200			
125	aag gag gcc gag aag aag gtg gtg atc aag agc gag gcg gcg tcc ccg	2894		
126	Lys Glu Ala Glu Lys Lys Val Val Ile Lys Ser Glu Ala Ala Ser Pro			
127	205 210 215 220			
129	gcg ctg ccg gtc atc acc aag gtg gag acg ctg agc ccc gag agc gcg	2942		
130	Ala Leu Pro Val Ile Thr Lys Val Glu Thr Leu Ser Pro Glu Ser Ala			
131	225 230 235			
133	ctg cag ggc agc ccg cgc agc gcg gcc tcc acg ccc gcc ggc tcc ccc	2990		
134	Leu Gln Gly Ser Pro Arg Ser Ala Ala Ser Thr Pro Ala Gly Ser Pro			
135	240 245 250			
137	gac ggt tcg ctg ccg gag cac cac gcc gcg gcg ccc aac ggg ctg cct	3038		
138	Asp Gly Ser Leu Pro Glu His His Ala Ala Ala Pro Asn Gly Leu Pro			
139	255 260 265			
141	ggc ttc agc gtg gag aac atc atg acc ctg cga acg tcg ccg ccg ggc	3086		
142	Gly Phe Ser Val Glu Asn Ile Met Thr Leu Arg Thr Ser Pro Pro Gly			
143	270 275 280			
145	gga gag ctg agc ccg ggg gcc gga cgc gcg ggc ctg gtg gtg ccg ccg	3134		
146	Gly Glu Leu Ser Pro Gly Ala Gly Arg Ala Gly Leu Val Val Pro Pro			
147	285 290 295 300			
149	ctg gcg ctg cca tac gcc gcc gcg ccg ccc gcc gcc tac ggc cag ccg	3182		
150	Leu Ala Leu Pro Tyr Ala Ala Ala Pro Pro Ala Ala Tyr Gly Gln Pro			
151	305 310 315			
153	tgc gct cag ggc ctg gag gcc ggg gcc gcc ggg ggc tac cag tgc agc	3230		
154	Cys Ala Gln Gly Leu Glu Ala Gly Ala Ala Gly Gly Tyr Gln Cys Ser			
155	320 325 330			
157	atg cga gcg atg agc ctg tac acc ggg gcc gag cgg ccg gcg cac atg	3278		
158	Met Arg Ala Met Ser Leu Tyr Thr Gly Ala Glu Arg Pro Ala His Met			
159	335 340 345			
161	tgc gtc ccg ccc gcc ctg gac gag gcc ctc tcg gac cac ccg agc ggc	3326		
162	Cys Val Pro Pro Ala Leu Asp Glu Ala Leu Ser Asp His Pro Ser Gly			
163	350 355 360			
165	ccc acg tcg ccc ctg agc gct ctc aac ctc gcc gcc ggc cag gag ggc	3374		
166	Pro Thr Ser Pro Leu Ser Ala Leu Asn Leu Ala Ala Gly Gln Glu Gly			
167	365 370 375 380			
169	gcg ctc gcc gcc acg ggc cac cac cac cag cac cac ggc cac cac cac	3422		
170	Ala Leu Ala Ala Thr Gly His His His Gln His His Gly His His His			
171	385 390 395			
173	ccg cag gcg ccg ccg ccc ccg ccg gct ccc cag ccc cag ccg acg ccg	3470		
174	Pro Gln Ala Pro Pro Pro Pro Pro Ala Pro Gln Pro Gln Pro Thr Pro			
175	400 405 410			
177	cag ccc ggg gcc gcc gcg gcg cag gcg gcc tcc tgg tat ctc aac cac	3518		
178	Gln Pro Gly Ala Ala Ala Ala Gln Ala Ala Ser Trp Tyr Leu Asn His			
179	415 420 425			
181	agc ggg gac ctg aac cac ctc ccc ggc cac acg ttc gcg gcc cag cag	3566		
182	Ser Gly Asp Leu Asn His Leu Pro Gly His Thr Phe Ala Ala Gln Gln			
183	430 435 440			

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185  caa act ttc ccc aac gtg cgg gag atg ttc aac tcc cac cgg ctg ggg      3614
186  Gln Thr Phe Pro Asn Val Arg Glu Met Phe Asn Ser His Arg Leu Gly
187  445                               450                               455                               460
189  att gag aac tcg acc ctc ggg gag tcc cag gtg agt ggc aat gcc agc      3662
190  ile Glu Asn Ser Thr Leu Gly Glu Ser Gln Val Ser Gly Asn Ala Ser
191                               465                               470                               475
193  tgc cag ctg ccc tac aga tcc acg ccg cct ctc tat cgc cac gca gcc      3710
194  Cys Gln Leu Pro Tyr Arg Ser Thr Pro Pro Leu Tyr Arg His Ala Ala
195                               480                               485                               490
197  ccc tac tcc tac gac tgc acg aaa tac tgacgtgtcc cgggacctcc      3757
198  Pro Tyr Ser Tyr Asp Cys Thr Lys Tyr
199                               495                               500
201  cctccccggc ccgctccggc ttcgcttccc agccccgacc caaccagaca attaaggggc      3817
202  tgcagagacg caaaaaagaa acaaaacatg tccaccaacc ttttctcaga cccgggagca      3877
203  gagagcgggc acgctagccc ccagccgtct gtgaagagcg caggtaactt taattcgccg      3937
204  ccccgtttct gggatcccag gaaacccctc caaagggacg cagcccaaca aaatgagtat      3997
205  tgggtcttaa atccccctcc cctaccagga cggctgtgct gtgctcgacc tgagctttca      4057
206  aaagttaagt tatggaccca aatcccatag cgagccccta gtgactttct gtagggttcc      4117
207  ccataggtgt atgggggtct ctatagataa tatatgtgct gtgtgtaatt ttaaatttct      4177
208  ccaaccgtgc tgtacaaatg tgtggatttg taatcaggct attttgttgt tgttgttgtt      4237
209  gttcagagcc attaatataa tatttaaaagt tgagttcact ggataagttt ttcactctgc      4297
210  ccaaccattt ctaactgcc aattgaattc aagaaaccga tgtgggtttt gtttcctgta      4357
211  caattatgag atataattct ttttccatt gttaggtctt tacaaaacaa gaaaataatt      4417
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213  atgggtttgt atagtaggtt ccaccctgag tattcctaaa agaaaaaaaa aaaaaaagct      4537
214  taaaaactct aacttcattc gtgtttgtct tacgtggtct taatcgttgt acttacctta      4597
215  aaataaaccc atgttgtttt ttctgccc aaagtttgaca gtgtgtttgt gttgttgcat      4657
216  tttttacaaa cgagggtgtg ttgcaaacc acctgctttg attatttttg ttacacaggt      4717
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220  tgcattttct taaatgcaca aaaacatgct aattgtcaaa acaaacagtg ccactccatc      4957
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225  gactttatta cttctcaatg tcatgtctaa atctacacc tcactgcagt gaaaaatttt      5257
226  aaaacctcat tacccttcaa aaataattta tgatattttt agagtcttaa attcaagttt      5317
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228  catttttaat agtaacatag tttttgtgaa atgtagctga cgaaatggct ttattatcta      5437
229  tttcaatggc tgaagtccac cactcccctg ctggcctcta tgtgtgaatt tggggacca      5497
230  agcttcatca attcccacc cagcagggtg gctgtacct gctaagtctg aagttctttg      5557
231  tgagcttaac gtttcaagac cagatgattt tgctaaaggt gattttgctt gatgcagtgg      5617
232  cgctgaacgt aaccgggtg tttttgtcgt gttgttttca acatggcact ttatctccac      5677
233  gctatgttga aatagaatta ggggaagctt aaagcataat aattgtcccc acatgtgcaa      5737
234  cacagactct ttcaatctgt ggccccagag gtggcacaca gttaagactt ggcggctgtc      5797
235  tcattctttt tcataatgtg cgggttcccg ggtgtccggg tgctagactt tcagcaggcc      5857
236  ccaggccaga cgggctttgg ttgagtgaac aggaggagg agttaaggag gtagggttgg      5917
237  ggagagaccc tctccaagct gcagaagaag gtggcccaag ctcccttgct gcgtctgccg      5977

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238 tgatggtttc attttacttc tgctcgcttc atgctatttg ccccaggaga agaggagagt 6037
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241 gagagacacg cggagaaata aaggagagcg acggtgtggc tgagagcccc caggtctgct 6217
242 gttgaaacta agctgggctt ttgcaccttt aggaagcctt tttaaagaag tcctgctgtg 6277
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244 ctccctgggg aacgtgggca acggggggat tgtatctgaa gctttattca ggtcttcggc 6397
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246 c 6458
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249 <211> LENGTH: 501
250 <212> TYPE: PRT
251 <213> ORGANISM: Homo sapiens
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255 1 5 10 15
256 Pro Tyr Leu Ser Glu Gln Asn Tyr Tyr Arg Ala Ala Gly Ser Tyr Gly
257 20 25 30
258 Gly Met Ala Ser Pro Met Gly Val Tyr Ser Gly His Pro Glu Gln Tyr
259 35 40 45
260 Ser Ala Gly Met Gly Arg Ser Tyr Ala Pro Tyr His His His Gln Pro
261 50 55 60
262 Ala Ala Pro Lys Asp Leu Val Lys Pro Pro Tyr Ser Tyr Ile Ala Leu
263 65 70 75 80
264 Ile Thr Met Ala Ile Gln Asn Ala Pro Glu Lys Lys Ile Thr Leu Asn
265 85 90 95
266 Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe Tyr Arg Glu Asn
267 100 105 110
268 Lys Gln Gly Trp Gln Asn Ser Ile Arg His Asn Leu Ser Leu Asn Glu
269 115 120 125
270 Cys Phe Val Lys Val Pro Arg Asp Asp Lys Lys Pro Gly Lys Gly Ser
271 130 135 140
272 Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn Met Phe Glu Asn Gly Ser
273 145 150 155 160
274 Phe Leu Arg Arg Arg Arg Arg Phe Lys Lys Lys Asp Val Ser Lys Glu
275 165 170 175
276 Lys Glu Glu Arg Ala His Leu Lys Glu Pro Pro Pro Ala Ala Ser Lys
277 180 185 190
278 Gly Ala Pro Ala Thr Pro His Leu Ala Asp Ala Pro Lys Glu Ala Glu
279 195 200 205
280 Lys Lys Val Val Ile Lys Ser Glu Ala Ala Ser Pro Ala Leu Pro Val
281 210 215 220
282 Ile Thr Lys Val Glu Thr Leu Ser Pro Glu Ser Ala Leu Gln Gly Ser
283 225 230 235 240
284 Pro Arg Ser Ala Ala Ser Thr Pro Ala Gly Ser Pro Asp Gly Ser Leu
285 245 250 255
286 Pro Glu His His Ala Ala Ala Pro Asn Gly Leu Pro Gly Phe Ser Val
287 260 265 270
288 Glu Asn Ile Met Thr Leu Arg Thr Ser Pro Pro Gly Gly Glu Leu Ser

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VERIFICATION SUMMARY

DATE: 10/10/2001

PATENT APPLICATION: US/09/963,285

TIME: 14:02:25

Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963285.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:554 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, EXON LOCATION:
(1649)...(438)